

125923

From: Kaufman, Claire
Sent: Tuesday, June 29, 2004 1:03 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/063,591

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX:Rem 4C70
Room:Rem 4E85 Serial #:10/063, ~~591~~ Date:6/29/04
115

Please search SEQ ID NO:81 and 82
in commercial databases.

Please put results on disk.

Thanks,
Claire Kaufman, AU 1646
Rem 4E85 (571) 272-0873

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

Medline & Biosis

=> s human chordin-like

L1 1 HUMAN CHORDIN-LIKE

=> d

L1 ANSWER 1 OF 1 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN

AN 2004:302643 BIOSIS

DN PREV200400303074

TI hCHL2, a novel chordin-related gene, displays differential expression and complex alternative splicing in human tissues and during myoblast and osteoblast maturation.

AU Oren, Anat; Toporik, Amir; Biton, Sharon; Almogy, Nechama; Eshel, Dani; Bernstein, Jeanne; Savitsky, Kinneret; Rotman, Galit [Reprint Author]

CS Compugen Ltd, 72 Pinchas Rosen St, IL-69512, Tel Aviv, Israel
galitr@compugen.co.il

SO Gene (Amsterdam), (April 28 2004) Vol. 331, No. April 28, pp. 17-31.
print.

ISSN: 0378-1119 (ISSN print).

DT Article

LA English

ED Entered STN: 30 Jun 2004

Last Updated on STN: 30 Jun 2004

Art Unit: 1646

LOCUS AI739159 601 bp mRNA linear EST 20-DEC-1999

DEFINITION wil8h06.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2390651 3' similar to SW:CA11_CHICK P02457 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR. ;, mRNA sequence.

ACCESSION AI739159

VERSION AI739159.1 GI:5101140

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 601)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 949 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 445.

FEATURES

source Location/Qualifiers

1. .601

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2390651"

/tissue_type="colon tumor, RER+"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Col6"

/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col10 was prepared, and ss circles were made in vitro. Following purification, this DNA was used as tracer in a hybridization reaction. The driver was PCR-amplified from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "

HAP

subtractive

cDNAs

Art Unit: 1646

ORIGIN

Query Match 34.0%; Score 588.2; DB 9; Length 601;
Best Local Similarity 98.7%; Pred. No. 2.5e-87;
Matches 593; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy      1112 CCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCC 1171
      || |||||
Db      601 CCATGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCAAGCGTGTGACCTGTCCC 542

Qy      1172 ACCGAGTACCCCTGCCGTCACCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCCCA 1231
      || |||||
Db      541 ACGAAGTACCCCTGCCGTCACCCGAGATAGTGGCTGGGAAGTGCTGCAAGATTGCCCCA 482

Qy      1232 GAGGACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCG 1291
      |||||
Db      481 GAGGACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCG 422

Qy      1292 GGCCGGGTCCTCGTCCACACATCGGTATCCCAAGCCCAGACAACCTGCGTCGCTTTGCC 1351
      |||||
Db      421 GGCCGGGTCCTCGTCCACACATCGGTATCCCAAGCCCAGACAACCTGCGTCGCTTTGCC 362

Qy      1352 CTGGAACACGAGGCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAG 1411
      |||||
Db      361 CTGGAACACGAGGCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAG 302

Qy      1412 GAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCA 1471
      |||||
Db      301 GAAACTGAGGCTCAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCA 242

Qy      1472 CTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCG 1531
      |||||
Db      241 CTTGACTCAGATCAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCG 182

Qy      1532 ACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCT 1591
      |||||
Db      181 ACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCT 122

Qy      1592 GAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAG 1651
      |||||
Db      121 GAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAG 62

Qy      1652 ATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGCATTACCCTCA 1711
      |||||
Db      61 ATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGCATAACCATCA 2

Qy      1712 A 1712
      |
Db      1 A 1
```

AW083466/c
 LOCUS AW083466 391 bp mRNA linear EST 14-OCT-1999
 DEFINITION xc02b12.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583071 3' similar to contains MER22.t1 MER22 repetitive element ;, mRNA sequence.
 ACCESSION AW083466
 VERSION AW083466.1 GI:6038542
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 391)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 368.
 FEATURES Location/Qualifiers
 source 1. .391
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2583071"
 /tissue_type="moderately differentiated adenocarcinoma"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Co21"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Normalized to Cot >500. Average insert size 1.04kb. Normalized version of NCI_CGAP_Col8. Library constructed by Life Technologies."

ORIGIN

Query Match 21.9%; Score 380; DB 9; Length 391;
 Best Local Similarity 99.7%; Pred. No. 6.8e-53;
 Matches 391; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

Qy      1010 ATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGGAAGACGTACTCCCAC 1069
          |||
Db      391 ATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGGAAGACGT-CTCCCAC 333

Qy      1070 GGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTGCATCCTATGCACC 1129
          |||
Db      332 GGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTGCATCCTATGCACC 273

Qy      1130 TGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGT 1189
          |||
Db      272 TGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGT 213

Qy      1190 CACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCGAGAGACAAAGCAGACCCT 1249
          |||

```

Db 212 CACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGACCCT 153

Qy 1250 GGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTCTCGTCCAC 1309
|||||

Db 152 GGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTCTCGTCCAC 93

Qy 1310 ACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCG 1369
|||||

Db 92 ACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTCG 33

Qy 1370 GACTTGGTGGAGATCTACCTCTGGAAGCTGGT 1401
|||||

Db 32 GACTTGGTGGAGATCTACCTCTGGAAGCTGGT 1

Art Unit: 1646

LOCUS AF332891 1047 bp mRNA linear HTC 13-JUL-2001
 DEFINITION Homo sapiens FKSG37 (FKSG37) mRNA, complete cds.
 ACCESSION AF332891
 VERSION AF332891.1 GI:12276190
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1047)
 AUTHORS Wang, Y.-G. and Gong, L.
 TITLE Cloning of FKSG37, a novel gene located on human chromosome 11q14
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1047)
 AUTHORS Wang, Y.-G.
 TITLE Direct Submission
 JOURNAL Submitted (01-JAN-2001) Beijing Fengkesheng Function Gene
 Technology Ltd., 4 Toutiao Lu Chang Street, Xuanwu District,
 Beijing 100050, P.R. China
 FEATURES Location/Qualifiers
 source 1..1047
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="11"
 /map="11q14"
 gene 1..1047
 /gene="FKSG37"
 CDS 121..966
 /gene="FKSG37"
 /codon_start=1
 /product="FKSG37"
 /protein_id="AAG50288.1"
 /db_xref="GI:12276191"

/translation="MYQHGEIFSAHELFP SRLPNQCVLCSTEGQIYCGLTTCPEPGC

PAPLPLPDSCCQACKAGSSWGLLCSVSDFHPSCHLQRHPQDPCSSDAGRKRGPPTAP

TGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYSHGEVWHPAFRAFGP

LPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKCKICPEDKADPGHSEISSTRCP

KAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKGI FLAQTLELKV TASPDKVTKT"

ORIGIN

Query Match 45.5%; Score 788.8; DB 11; Length 1047;
 Best Local Similarity 94.5%; Pred. No. 1.6e-120;
 Matches 830; Conservative 0; Mismatches 42; Indels 6; Gaps 1;

Qy 535 GCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGG 594
 || || | ||||||||||||||||||||||||||||||||||||||||
 Db 21 GCAGGTTGTGAGGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGG 80

Qy 595 ACTCCGGGCCCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAGAGAT 654
 ||||||||||||||||||||||||||||||||||||||||
 Db 81 ACTCCGGGCCCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAGAGAT 140

Qy	655	CTTCAGTGCCCATGAGCTGTTCCCTTCCCGCTGCCCAACCAAGTGTGTCTCTGCAGCTG	714
Db	141	CTTCAGTGCCCATGAGCTGTTCCCTTCCCGCTGCCCAACCAAGTGTGTCTCTGCAGCTG	200
Qy	715	CACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACC	774
Db	201	CACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCCAGCACC	260
Qy	775	CCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAA-----GTGAGCA	828
Db	261	CCTCCCGCTGCCAGACTCCTGCTGCCAGGCCTGCAAAGCTGGCTCCAGCTGGGGCCTGCT	320
Qy	829	ATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATG	888
Db	321	ATGCTCAGTCAGTGACTTTCATCCTTCCTGCCATTTGCAGAGACATCCTCAGGATCCATG	380
Qy	889	TTCCAGTGATGCTGGGAGAAAAGAGAGGCCCGGGCACCCAGCCCCACTGGCCTCAGCGC	948
Db	381	TTCCAGTGATGCTGGGAGAAAAGAGAGGCCCGGGCACCCAGCCCCACTGGCCTCAGCGC	440
Qy	949	CCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACCTGTCAA	1008
Db	441	CCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACCTGTCAA	500
Qy	1009	GATCGTCCTGAAGGAGAAAACATAAGAAAGCCTGTGTGCATGGCGGGAAGACGTA	1068
Db	501	GATCGTCCTGAAGGAGAAAACATAAGAAAGCCTGTGTGCATGGCGGGAAGACGTA	560
Qy	1069	CGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCTGCATCCTATGCAC	1128
Db	561	CGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCTGCATCCTATGCAC	620
Qy	1129	CTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCG	1188
Db	621	CTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCG	680
Qy	1189	TCACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCCAGAGGACAAAGCAGACCC	1248
Db	681	TCACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCCAGAGGACAAAGCAGACCC	740
Qy	1249	TGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCCTCGTCCA	1308
Db	741	TGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCCTCGTCCA	800
Qy	1309	CACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTC	1368
Db	801	CACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGCCTC	860
Qy	1369	GGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAG	1406
Db	861	GGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAG	898

LOCUS AY163868 1368 bp mRNA linear PRI 15-JUL-2003
DEFINITION Homo sapiens BNF1 mRNA, complete cds.
ACCESSION AY163868
VERSION AY163868.1 GI:32492075
KEYWORDS .

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1368)
AUTHORS Wu, I. and Moses, M.A.
TITLE BNF-1, a novel gene encoding a putative extracellular matrix
protein, is overexpressed in tumor tissues
JOURNAL Gene 311 (C), 105-110 (2003)
PUBMED 12853144
REFERENCE 2 (bases 1 to 1368)
AUTHORS Wu, I. and Moses, M.A.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2002) Surgical Research, The Children's Hospital,
320 Longwood Ave., Boston, MA 02115, USA

FEATURES Location/Qualifiers
source 1..1368
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
CDS 4..1359
/codon_start=1
/product="BNF1"
/protein_id="AA031809.1"
/db_xref="GI:32492076"
/translation="MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGE
SWHPYLEPQGLMYCLRCTCSEGAHVSCYRLHCPVHCPQPVTEPQQCCPKCVPHTPS
GLRAPPKSCQHNGTMYQHGEIFSAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGC
PAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVVRHPQDPCSSDAGRKRGPPTAPTG
LSAPLSFI PRHFRPKGAGSTTVKI VLKEKHKKACVHGGKTYSHGEVWHPAFRAFGPLP
CILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKCKICPEDKADPGHSEISSTRCPKA
PGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPHSQ
NLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPGAEGHGQSRQSDQDITK
T"

ORIGIN

Query Match 79.0%; Score 1368; DB 9; Length 1368;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      284 AGGATGGTTCCCGAGGTGAGGGTCCTCTCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTC 343
          |||
Db       1 AGGATGGTTCCCGAGGTGAGGGTCCTCTCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTC 60

Qy      344 CCCCTGGACTCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTTCCATGGGAAGAGA 403
          |||
Db       61 CCCCTGGACTCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTTCCATGGGAAGAGA 120

Qy      404 TACTCCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGTACTGCCTG 463
          |||
Db      121 TACTCCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGTACTGCCTG 180
```

Qy	464	CGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTC	523
Db	181	CGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTC	240
Qy	524	CACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCAC	583
Db	241	CACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCAC	300
Qy	584	ACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAA	643
Db	301	ACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAA	360
Qy	644	CACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGTC	703
Db	361	CACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCCCGCCTGCCCAACCAGTGTGTC	420
Qy	704	CTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGC	763
Db	421	CTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGC	480
Qy	764	TGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGT	823
Db	481	TGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGT	540
Qy	824	GAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGAT	883
Db	541	GAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGAT	600
Qy	884	CCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCCGGGCACCCAGCCCCCACTGGCCTC	943
Db	601	CCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCCGGGCACCCAGCCCCCACTGGCCTC	660
Qy	944	AGCGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACT	1003
Db	661	AGCGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAGGCAGCACAACT	720
Qy	1004	GTCAAGATCGTCCTGAAGGAGAAACATAAGAAAAGCCTGTGTGCATGGCGGGAAGACGTAC	1063
Db	721	GTCAAGATCGTCCTGAAGGAGAAACATAAGAAAAGCCTGTGTGCATGGCGGGAAGACGTAC	780
Qy	1064	TCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTGCATCCTA	1123
Db	781	TCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTGCATCCTA	840
Qy	1124	TGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCCC	1183
Db	841	TGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCCC	900
Qy	1184	TGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGTCTGCAAGATTTGCCAGAGGACAAAGCA	1243
Db	901	TGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGTCTGCAAGATTTGCCAGAGGACAAAGCA	960
Qy	1244	GACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTCTC	1303
Db	961	GACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTCTC	1020
Qy	1304	GTCCACACATCGGTATCCCCAAGCCCAGACAACTGCGTCGCTTTGCCCCTGGAACACGAG	1363

Db	1021		GTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAG	1080
Qy	1364		GCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAAGATGAGGAAACTGAGGCT	1423
Db	1081		GCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAAGATGAGGAAACTGAGGCT	1140
Qy	1424		CAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGAT	1483
Db	1141		CAGAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGAT	1200
Qy	1484		CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGG	1543
Db	1201		CAAGAAAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGG	1260
Qy	1544		CCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTCACGGC	1603
Db	1261		CCCCCACGAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTCACGGC	1320
Qy	1604		CAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAG	1651
Db	1321		CAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAG	1368

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 13:40:34 ; Search time 4714 Seconds
(without alignments)
10971.849 Million cell updates/sec

Title: US-10-063-591-81
Perfect score: 1732
Sequence: 1 cccacgcgtccgcgcctctc.....aaaaaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
	1	788.8	45.5	1047	11	AF332891	AF332891 Homo sapi
	2	735	42.4	1485	11	AK007577	AK007577 Mus muscu
c	3	588.2	34.0	601	9	AI739159	AI739159 wi18h06.x
	4	513	29.6	525	13	BX480331	BX480331 DKFZp686G
	5	477.8	27.6	481	13	BX091758	BX091758 BX091758
	6	429.8	24.8	545	12	BI774183	BI774183 466194 MA
	7	423	24.4	424	9	AL047873	AL047873 DKFZp586M
	8	422.4	24.4	756	12	BI112782	BI112782 602898795
	9	405.8	23.4	768	12	BI113110	BI113110 602898895
	10	389.8	22.5	915	10	BE911015	BE911015 601662108
c	11	380	21.9	391	9	AW083466	AW083466 xc02b12.x
	12	379.2	21.9	474	10	BF653749	BF653749 277683 MA
	13	359	20.7	942	12	BI456773	BI456773 603174663
c	14	343.8	19.8	421	9	AA040433	AA040433 zk46c09.s
	15	341.6	19.7	716	10	BF134285	BF134285 601784261
c	16	329	19.0	329	9	AI205645	AI205645 qg30g03.x
	17	300.4	17.3	629	12	BI067140	BI067140 pgfln.pk0
	18	294.6	17.0	352	10	AW482630	AW482630 46339 MAR
c	19	285	16.5	667	13	BQ181634	BQ181634 UI-H-EU0-
	20	279.2	16.1	373	10	AW425392	AW425392 57293 MAR
c	21	272.8	15.8	398	9	AA042913	AA042913 zk56e08.s
c	22	271	15.6	294	14	CB047807	CB047807 NISC_gj01
	23	270.2	15.6	368	10	AW356676	AW356676 39202 MAR
	24	270	15.6	294	14	CB047808	CB047808 NISC_gj01
	25	267.4	15.4	750	12	BG175998	BG175998 602335223
c	26	259.4	15.0	348	9	AA037778	AA037778 zk38f06.s
	27	259.4	15.0	376	9	AV661482	AV661482 AV661482
c	28	254.4	14.7	347	9	AI343625	AI343625 qp11b04.x
	29	250.8	14.5	452	10	BE629331	BE629331 uu36f11.y
c	30	228	13.2	228	10	BF437134	BF437134 7p63f11.x
c	31	226.4	13.1	228	10	BF437637	BF437637 7p78d05.x
c	32	225.2	13.0	450	12	BI286468	BI286468 UI-R-DE0-
c	33	222.8	12.9	442	10	BE629653	BE629653 uu36f11.x
	34	200.4	11.6	770	10	BF181980	BF181980 601805915
	35	190.6	11.0	248	9	AA040432	AA040432 zk46c09.r
	36	181.6	10.5	472	9	AA514464	AA514464 nf57f02.s
	37	181.4	10.5	476	10	BF354695	BF354695 RC0-HT077
	38	179.4	10.4	426	10	BF354693	BF354693 RC0-HT077
	39	177.6	10.3	275	9	AA042926	AA042926 zk56e08.r
	40	175.2	10.1	245	9	AA040904	AA040904 zk38f06.r
	41	171	9.9	939	13	BU514386	BU514386 AGENCOURT
	42	157	9.1	855	10	BE799088	BE799088 601588485
c	43	155.2	9.0	1201	13	BX381985	BX381985 BX381985
	44	154.6	8.9	1201	13	BX381986	BX381986 BX381986
	45	153.4	8.9	275	10	BB513170	BB513170 BB513170

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 15:24:44 ; Search time 800 Seconds
(without alignments)
10444.409 Million cell updates/sec

Title: US-10-063-591-81
Perfect score: 1732
Sequence: 1 cccacgcgtccgcgcctctc.....aaaaaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	1732	100.0	1732	10	US-09-946-374-141	Sequence 141, App
2	1732	100.0	1732	12	US-10-015-395A-141	Sequence 141, App
3	1732	100.0	1732	13	US-10-206-915-281	Sequence 281, App
4	1732	100.0	1732	13	US-10-199-670-281	Sequence 281, App
5	1732	100.0	1732	13	US-10-201-858-281	Sequence 281, App
6	1732	100.0	1732	13	US-10-205-890-281	Sequence 281, App
7	1732	100.0	1732	13	US-10-208-024-281	Sequence 281, App
8	1732	100.0	1732	13	US-10-201-853-281	Sequence 281, App
9	1732	100.0	1732	13	US-10-063-745-81	Sequence 81, Appl
10	1732	100.0	1732	13	US-10-063-512-81	Sequence 81, Appl
11	1732	100.0	1732	13	US-10-063-513-81	Sequence 81, Appl
12	1732	100.0	1732	13	US-10-063-515-81	Sequence 81, Appl
13	1732	100.0	1732	13	US-10-063-549-81	Sequence 81, Appl
14	1732	100.0	1732	13	US-10-063-569-81	Sequence 81, Appl
15	1732	100.0	1732	13	US-10-063-551-81	Sequence 81, Appl
16	1732	100.0	1732	13	US-10-174-581-281	Sequence 281, App
17	1732	100.0	1732	13	US-10-176-483-281	Sequence 281, App
18	1732	100.0	1732	13	US-10-176-749-281	Sequence 281, App
19	1732	100.0	1732	13	US-10-176-914-281	Sequence 281, App
20	1732	100.0	1732	13	US-10-176-915-281	Sequence 281, App
21	1732	100.0	1732	13	US-10-006-485A-141	Sequence 141, App
22	1732	100.0	1732	13	US-10-013-907A-141	Sequence 141, App
23	1732	100.0	1732	13	US-10-015-499A-141	Sequence 141, App
24	1732	100.0	1732	13	US-10-063-555-81	Sequence 81, Appl
25	1732	100.0	1732	13	US-10-063-563-81	Sequence 81, Appl
26	1732	100.0	1732	13	US-10-063-594-81	Sequence 81, Appl
27	1732	100.0	1732	13	US-10-063-553-81	Sequence 81, Appl
28	1732	100.0	1732	13	US-10-063-554-81	Sequence 81, Appl
29	1732	100.0	1732	13	US-10-176-484-281	Sequence 281, App
30	1732	100.0	1732	13	US-10-180-550-281	Sequence 281, App
31	1732	100.0	1732	13	US-10-183-014-281	Sequence 281, App
32	1732	100.0	1732	13	US-10-187-738-281	Sequence 281, App
33	1732	100.0	1732	13	US-10-187-740-281	Sequence 281, App
34	1732	100.0	1732	13	US-10-187-883-281	Sequence 281, App
35	1732	100.0	1732	13	US-10-194-363-281	Sequence 281, App
36	1732	100.0	1732	13	US-10-194-460-281	Sequence 281, App
37	1732	100.0	1732	13	US-10-194-463-281	Sequence 281, App
38	1732	100.0	1732	13	US-10-194-484-281	Sequence 281, App
39	1732	100.0	1732	13	US-10-195-884-281	Sequence 281, App
40	1732	100.0	1732	13	US-10-195-896-281	Sequence 281, App
41	1732	100.0	1732	13	US-10-196-744-281	Sequence 281, App
42	1732	100.0	1732	13	US-10-196-755-281	Sequence 281, App
43	1732	100.0	1732	13	US-10-196-757-281	Sequence 281, App
44	1732	100.0	1732	13	US-10-197-704-281	Sequence 281, App
45	1732	100.0	1732	13	US-10-197-710-281	Sequence 281, App

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 15:12:54 ; Search time 135 Seconds
(without alignments)
7119.814 Million cell updates/sec

Title: US-10-063-591-81
Perfect score: 1732
Sequence: 1 cccacgcgtccgcgcctctc.....aaaaaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	ID DB	Description
	1	1501.8	86.7	1570	4	US-09-798-051-4
	2	822.4	47.5	1839	4	US-09-798-051-1
c	3	196.4	11.3	2315	4	US-09-152-060-48
	4	194.2	11.2	3856	4	US-09-620-312D-451
	5	102	5.9	7218	1	US-08-232-463-14
	6	88.8	5.1	1732	4	US-09-152-060-30
	7	60.2	3.5	507	4	US-09-489-039A-1200
c	8	60.2	3.5	516	4	US-09-489-039A-1064
c	9	60.2	3.5	537	4	US-09-489-039A-1065
c	10	60.2	3.5	549	4	US-09-489-039A-1130
	11	60.2	3.5	558	4	US-09-489-039A-1011

	12	60.2	3.5	609	4	US-09-489-039A-1177	Sequence 1177, Ap
	13	58	3.3	4897	6	5196516-7	Patent No. 5196516
	14	57	3.3	53526	3	US-08-658-136-2	Sequence 2, Appli
	15	57	3.3	53577	3	US-08-658-136-1	Sequence 1, Appli
	16	55.2	3.2	1166	4	US-09-072-596-323	Sequence 323, App
	17	55.2	3.2	1166	4	US-09-072-967-328	Sequence 328, App
c	18	51.4	3.0	554	4	US-09-489-039A-1758	Sequence 1758, Ap
c	19	51.4	3.0	570	4	US-09-489-039A-1676	Sequence 1676, Ap
c	20	49.8	2.9	1559	3	US-09-019-095A-7	Sequence 7, Appli
	21	49.6	2.9	44453	4	US-09-146-053-5	Sequence 5, Appli
c	22	48.8	2.8	1926	4	US-09-249-585A-2	Sequence 2, Appli
c	23	48.8	2.8	1926	4	US-09-410-399-3	Sequence 3, Appli
c	24	48.8	2.8	2580	3	US-09-050-863-2	Sequence 2, Appli
c	25	48.8	2.8	2580	4	US-09-359-081-2	Sequence 2, Appli
	26	48.8	2.8	5452	2	US-09-130-114-1	Sequence 1, Appli
	27	48.8	2.8	8705	4	US-09-647-344A-14	Sequence 14, Appl
c	28	48.8	2.8	9600	3	US-08-910-647-1	Sequence 1, Appli
c	29	48.8	2.8	9600	4	US-09-620-925-1	Sequence 1, Appli
c	30	48.8	2.8	10596	1	US-07-884-811-15	Sequence 15, Appl
c	31	48.8	2.8	10596	1	US-07-885-971-15	Sequence 15, Appl
c	32	48.8	2.8	10596	1	US-08-087-783A-15	Sequence 15, Appl
c	33	48.8	2.8	10596	1	US-08-194-088B-15	Sequence 15, Appl
c	34	48.8	2.8	10596	2	US-08-194-087-15	Sequence 15, Appl
c	35	48.8	2.8	10596	5	PCT-US93-04648-15	Sequence 15, Appl
	36	48.8	2.8	16080	4	US-09-724-566A-48	Sequence 48, Appl
	37	48	2.8	66804	4	US-09-740-041-3	Sequence 3, Appli
c	38	47.6	2.7	473	4	US-09-621-976-14118	Sequence 14118, A
	39	47.6	2.7	703	3	US-09-313-300-6	Sequence 6, Appli
c	40	47.6	2.7	1377	2	US-08-810-572A-1	Sequence 1, Appli
c	41	47.6	2.7	1377	4	US-09-290-333-1	Sequence 1, Appli
c	42	47.6	2.7	1377	4	US-09-782-857A-1	Sequence 1, Appli
c	43	47.6	2.7	1377	4	US-09-879-919-21	Sequence 21, Appl
	44	46.4	2.7	505	4	US-09-621-976-15639	Sequence 15639, A
c	45	45.8	2.6	289	3	US-09-007-005-17	Sequence 17, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 13:32:29 ; Search time 708 Seconds
(without alignments)
10392.485 Million cell updates/sec

Title: US-10-063-591-81
Perfect score: 1732
Sequence: 1 cccacgcgtccgcgcctctc.....aaaaaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002s:*
- 7: geneseqn2003as:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1732	100.0	1732	3	AAA37064	Aaa37064 Human PRO
2	1732	100.0	1732	4	AAF54300	Aaf54300 DNA encod
3	1732	100.0	1732	4	AAF92098	Aaf92098 Human PRO
4	1732	100.0	1732	6	ABS74418	Abs74418 Human cDN
5	1732	100.0	1732	7	ABX78668	Abx78668 Human PRO
6	1732	100.0	1732	7	ACA75640	Aca75640 Novel hum
7	1732	100.0	1732	7	ACA71120	Aca71120 Human sec

8	1732	100.0	1732	7	ACC87648	Acc87648	Human	sec
9	1732	100.0	1732	7	ACC87034	Acc87034	Human	sec
10	1732	100.0	1732	7	ACD04207	Acd04207	Human	sec
11	1732	100.0	1732	7	ACA69538	Aca69538	cDNA	enco
12	1732	100.0	1732	7	ACA90383	Aca90383	Novel	hum
13	1732	100.0	1732	7	ACC89490	Acc89490	Human	sec
14	1732	100.0	1732	7	ACA98281	Aca98281	Novel	hum
15	1732	100.0	1732	7	ACA93923	Aca93923	Human	sec
16	1732	100.0	1732	7	ACD15316	Acd15316	Human	sec
17	1732	100.0	1732	7	ACD08903	Acd08903	Human	sec
18	1732	100.0	1732	7	ACC96823	Acc96823	Human	sec
19	1732	100.0	1732	7	ACF15544	Acf15544	Human	sec
20	1732	100.0	1732	7	ACA72911	Aca72911	Human	PRO
21	1732	100.0	1732	7	ACD03083	Acd03083	Novel	hum
22	1732	100.0	1732	7	ACD01898	Acd01898	Novel	hum
23	1732	100.0	1732	7	ACA92090	Aca92090	Novel	hum
24	1732	100.0	1732	7	ACA89515	Aca89515	cDNA	enco
25	1732	100.0	1732	7	ACA73525	Aca73525	Human	sec
26	1732	100.0	1732	7	ACA05840	Aca05840	Human	sec
27	1732	100.0	1732	7	ACA66674	Aca66674	cDNA	enco
28	1732	100.0	1732	7	ACA91204	Aca91204	Novel	hum
29	1732	100.0	1732	7	ACD81581	Acd81581	Human	CDN
30	1732	100.0	1732	7	ACF20249	Acf20249	Human	sec
31	1732	100.0	1732	7	ACF19635	Acf19635	Human	sec
32	1732	100.0	1732	7	ACD21923	Acd21923	Human	sec
33	1732	100.0	1732	7	ACF13088	Acf13088	Human	sec
34	1732	100.0	1732	7	ACD25191	Acd25191	Human	sec
35	1732	100.0	1732	7	ACF00240	Acf00240	Human	sec
36	1732	100.0	1732	7	ACA60403	Aca60403	Novel	hum
37	1732	100.0	1732	7	ACA72297	Aca72297	Novel	hum
38	1732	100.0	1732	7	ACD04821	Acd04821	Novel	hum
39	1732	100.0	1732	7	ACD18282	Acd18282	Human	sec
40	1732	100.0	1732	7	ACD08289	Acd08289	Human	sec
41	1732	100.0	1732	7	ACA88723	Aca88723	Novel	hum
42	1732	100.0	1732	7	ACA70165	Aca70165	Human	sec
43	1732	100.0	1732	7	ACD12387	Acd12387	Novel	hum
44	1732	100.0	1732	7	ACC74302	Acc74302	Human	sec
45	1732	100.0	1732	7	ACD15930	Acd15930	Human	sec

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 13:34:39 ; Search time 6945 Seconds
(without alignments)
10809.235 Million cell updates/sec

Title: US-10-063-591-81
Perfect score: 1732
Sequence: 1 cccacgcgtccgcgcctctc.....aaaaaaaaaaaaaaaaaaaaa 1732

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1732	100.0	1732	6	AX092350		AX092350	Sequence
	2	1732	100.0	1732	6	AX376214		AX376214	Sequence
	3	1732	100.0	1732	6	AX697073		AX697073	Sequence
	4	1732	100.0	1732	9	AY358522		AY358522	Homo sapi
	5	1720	99.3	1720	6	BD276565		BD276565	EXTRACELL
	6	1720	99.3	1720	6	AX048199		AX048199	Sequence
	7	1718	99.2	1738	6	AX363203		AX363203	Sequence
	8	1703.4	98.3	1792	6	AX119273		AX119273	Sequence
	9	1694	97.8	1722	6	AX140200		AX140200	Sequence
	10	1687.6	97.4	1722	6	AX140199		AX140199	Sequence
	11	1661	95.9	1722	6	AX140196		AX140196	Sequence
	12	1501.8	86.7	1570	6	AR409072		AR409072	Sequence
	13	1501.8	86.7	1570	6	AX235836		AX235836	Sequence
	14	1368	79.0	1368	9	AY163868		AY163868	Homo sapi
	15	1354.8	78.2	1356	6	AX119269		AX119269	Sequence
	16	1342.8	77.5	1817	6	AX140202		AX140202	Sequence
	17	1336.8	77.2	1405	6	AX363199		AX363199	Sequence
	18	1336	77.1	1517	6	AX363201		AX363201	Sequence
	19	1320.2	76.2	1890	6	AX140198		AX140198	Sequence
	20	1251.6	72.3	1281	6	AX140195		AX140195	Sequence
	21	1223.8	70.7	1290	6	AX119271		AX119271	Sequence
	22	1134.4	65.5	1515	6	AX140201		AX140201	Sequence
	23	1116.6	64.5	1515	6	AX140197		AX140197	Sequence
	24	942.8	54.4	1622	6	AX140203		AX140203	Sequence
	25	835.2	48.2	1516	10	BC019399		BC019399	Mus muscu
	26	822.8	47.5	1567	6	AX140204		AX140204	Sequence
	27	822.4	47.5	1839	6	AR409071		AR409071	Sequence
	28	822.4	47.5	1839	6	AX235833		AX235833	Sequence
	29	796.6	46.0	1428	10	AF338222		AF338222	Mus muscu
c	30	678.6	39.2	807	6	AX014311		AX014311	Sequence
c	31	678.6	39.2	807	6	BD222190		BD222190	Human nuc
	32	519	30.0	683	9	HSM800814		AL110168	Homo sapi
	33	424.8	24.5	1202	6	AX140205		AX140205	Sequence
	34	359.4	20.8	422	6	AX014296		AX014296	Sequence

	35	359.4	20.8	422	6	BD222175	BD222175 Human nuc
	36	357	20.6	141937	2	AC011686	AC011686 Homo sapi
c	37	357	20.6	230157	9	AP001324	AP001324 Homo sapi
c	38	343.8	19.8	421	6	AX337465	AX337465 Sequence
	39	244	14.1	211452	2	AP002010	AP002010 Homo sapi
	40	216	12.5	3827	6	AX175123	AX175123 Sequence
	41	211.4	12.2	1864	6	AX175120	AX175120 Sequence
	42	211.4	12.2	3291	10	AF296451	AF296451 Mus muscu
	43	210.2	12.1	1803	10	AF321853	AF321853 Mus muscu
	44	208.6	12.0	3601	10	BC050818	BC050818 Mus muscu
	45	208.2	12.0	2750	10	AF305714	AF305714 Mus muscu

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 20:43:33 ; Search time 46 Seconds
(without alignments)
3093.450 Million cell updates/sec

Title: US-10-063-591-82
Perfect score: 2545
Sequence: 1 MVPEVRVLSSLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	2545	100.0	451	4	Q7Z5J3	Q7z5j3 homo sapien
2	1549	60.9	426	11	Q8VEA6	Q8vea6 mus musculu
3	1542	60.6	406	11	Q925I3	Q925i3 mus musculu
4	1342	52.7	281	4	Q9BZ90	Q9bz90 homo sapien
5	959	37.7	194	4	Q9UG17	Q9ug17 homo sapien
6	793	31.2	448	4	Q7Z6V6	Q7z6v6 homo sapien
7	346.5	13.6	2327	13	Q9IBG7	Q9ibg7 xenopus lae
8	321.5	12.6	413	4	Q8N2W7	Q8n2w7 homo sapien
9	304	11.9	1027	13	Q7T3Q2	Q7t3q2 brachydanio
10	299.5	11.8	1028	11	Q9JLL0	Q9jll0 mus musculu
11	299	11.7	1048	13	Q8Aww5	Q8aww5 gallus gall
12	298	11.7	1036	4	Q9NZV1	Q9nzv1 homo sapien
13	295	11.6	955	4	Q96DN2	Q96dn2 homo sapien
14	292	11.5	673	4	Q86WK8	Q86wk8 homo sapien
15	281.5	11.1	940	13	O57465	O57465 gallus gall
16	255.5	10.0	4010	11	Q80T14	Q80t14 mus musculu
17	252	9.9	565	4	Q8TF36	Q8tf36 homo sapien
18	252	9.9	685	4	Q8N8U9	Q8n8u9 homo sapien
19	250	9.8	685	11	Q7TN57	Q7tn57 mus musculu
20	248	9.7	898	5	Q8MQG2	Q8mqg2 caenorhabdi
21	248	9.7	909	5	Q17429	Q17429 caenorhabdi
22	248	9.7	960	5	Q8MM07	Q8mm07 caenorhabdi
23	246.5	9.7	751	5	Q9GYX3	Q9gyx3 drosophila
24	246.5	9.7	751	5	Q9W2H2	Q9w2h2 drosophila
25	246	9.7	984	5	Q964I1	Q964i1 halocynthia
26	242	9.5	685	11	Q8CJ69	Q8cj69 mus musculu
27	237.5	9.3	651	4	Q86UZ4	Q86uz4 homo sapien
28	237.5	9.3	4007	4	Q86XX4	Q86xx4 homo sapien
29	212.5	8.3	608	11	Q80V54	Q80v54 mus musculu
30	210	8.3	286	11	Q8BS96	Q8bs96 mus musculu
31	190	7.5	1637	6	Q9XSV8	Q9xsv8 bos taurus
32	190	7.5	5146	6	Q8SPM4	Q8spm4 bos taurus
33	184.5	7.2	1354	5	Q9VKA7	Q9vka7 drosophila
34	179.5	7.1	4998	11	Q8CG65	Q8cg65 mus musculu
35	176	6.9	429	5	Q09538	Q09538 caenorhabdi
36	176	6.9	816	11	Q8R417	Q8r417 rattus norv
37	176	6.9	894	11	O88715	O88715 mus musculu
38	176	6.9	1350	11	Q80Z20	Q80z20 mus musculu
39	175	6.9	1034	11	O35888	O35888 rattus norv
40	174	6.8	2768	5	Q9VC00	Q9vc00 drosophila
41	173.5	6.8	324	11	Q8C8N3	Q8c8n3 mus musculu
42	170	6.7	5374	11	Q99ND0	Q99nd0 mus musculu
43	169	6.6	685	6	Q9TTS5	Q9tts5 bos taurus
44	168.5	6.6	284	5	Q8T1D1	Q8t1d1 dictyosteli
45	167.5	6.6	4123	4	O75851	O75851 homo sapien

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 20:40:23 ; Search time 17 Seconds
(without alignments)
1381.391 Million cell updates/sec

Title: US-10-063-591-82
Perfect score: 2545
Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	819	32.2	450	1	NRL1_HUMAN	Q9bu40 homo sapien
2	815	32.0	447	1	NRL1_MOUSE	Q920c1 mus musculu
3	806.5	31.7	456	1	NRL1_CHICK	Q90zd5 gallus gall
4	339.5	13.3	940	1	CHRD_BRARE	O57472 brachydanio
5	322	12.7	941	1	CHRD_XENLA	Q91713 xenopus lae
6	321.5	12.6	955	1	CHRD_HUMAN	Q9h2x0 homo sapien
7	288	11.3	948	1	CHRD_MOUSE	Q9z0e2 mus musculu
8	258.5	10.2	1038	1	SOG_DROME	Q24025 drosophila
9	194.5	7.6	2482	1	VWF_PIG	Q28833 sus scrofa
10	186	7.3	1693	1	SAS_DROME	Q04164 drosophila
11	184	7.2	816	1	NEL2_RAT	Q62918 rattus norv
12	178	7.0	5703	1	MU5B_HUMAN	Q9hc84 homo sapien
13	177	7.0	2813	1	VWF_HUMAN	P04275 homo sapien
14	170	6.7	810	1	NEL1_HUMAN	Q92832 homo sapien
15	169	6.6	5376	1	ZAN_MOUSE	O88799 mus musculu
16	165	6.5	354	1	NOV_MOUSE	Q64299 mus musculu
17	163.5	6.4	1262	1	CA13_CHICK	P12105 gallus gall

18	161	6.3	816	1	NEL2_HUMAN	Q99435	homo sapien
19	161	6.3	2813	1	VWF_CANFA	Q28295	canis famil
20	158.5	6.2	1466	1	CA13_HUMAN	P02461	homo sapien
21	158	6.2	816	1	NEL2_MOUSE	Q61220	mus musculu
22	158	6.2	1453	1	CA11_CHICK	P02457	gallus gall
23	156.5	6.1	176	1	CHRD_RAT	Q63148	rattus norv
24	156.5	6.1	1453	1	CA11_MOUSE	P11087	mus musculu
25	156	6.1	810	1	NEL1_RAT	Q62919	rattus norv
26	154.5	6.1	816	1	NEL_CHICK	Q90827	gallus gall
27	154	6.1	1184	1	FBL2_HUMAN	P98095	homo sapien
28	153.5	6.0	3133	1	HMCT_BOMMO	P98092	bombyx mori
29	152.5	6.0	375	1	CE10_CHICK	P19336	gallus gall
30	152	6.0	351	1	NOV_RAT	Q9qzq5	rattus norv
31	152	6.0	357	1	NOV_HUMAN	P48745	homo sapien
32	150	5.9	1460	1	CA11_CANFA	Q9xsj7	canis famil
33	149	5.9	1170	1	TSP2_BOVIN	Q95116	bos taurus
34	148.5	5.8	1238	1	JAG2_HUMAN	Q9y219	homo sapien
35	146.5	5.8	349	1	CTGF_BOVIN	O18739	bos taurus
36	146.5	5.8	1464	1	CA13_MOUSE	P08121	mus musculu
37	146	5.7	349	1	CTGF_HUMAN	P29279	homo sapien
38	146	5.7	867	1	SSPO_BOVIN	P98167	bos taurus
39	146	5.7	1247	1	JAG2_MOUSE	Q9qye5	mus musculu
40	144	5.7	1464	1	CA11_HUMAN	P02452	homo sapien
41	142.5	5.6	1496	1	CA25_HUMAN	P05997	homo sapien
42	141.5	5.6	699	1	ECM2_HUMAN	O94769	homo sapien
43	141	5.5	250	1	WSP2_RAT	Q9jhc6	rattus norv
44	141	5.5	1172	1	TSP2_HUMAN	P35442	homo sapien
45	140.5	5.5	250	1	WSP2_HUMAN	O76076	homo sapien

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 20:44:29 ; Search time 20 Seconds
(without alignments)
2169.119 Million cell updates/sec

Title: US-10-063-591-82
Perfect score: 2545
Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	959	37.7	194	2	T14746	hypothetical prote
2	322	12.7	941	1	A55195	chordin precursor
3	258.5	10.2	1038	2	T13177	sog protein - frui
4	248	9.7	884	2	T18649	hypothetical prote
5	187	7.3	1348	2	S27812	probable epidermal
6	187	7.3	1348	2	A43917	probable epidermal
7	177	7.0	2813	1	VWHU	von Willebrand fac
8	176	6.9	429	2	T21113	hypothetical prote
9	175	6.9	1034	2	JC5598	mucin - rat
10	169	6.6	5376	2	T42215	zonadhesin - mouse
11	163.5	6.4	886	2	I50694	collagen alpha 1(I
12	158.5	6.2	1466	1	CGHU7L	collagen alpha 1(I
13	158	6.2	615	2	A05269	collagen alpha 1(I

14	157.5	6.2	206	2	S18250	collagen alpha 1(I
15	156.5	6.1	1453	2	S21626	collagen alpha 1(I
16	156	6.1	810	2	T10756	Nel-homolog protei
17	155	6.1	153	2	A27179	collagen alpha 1(I
18	154	6.1	1184	2	A55184	fibulin-2 precurs
19	153.5	6.0	3133	2	S52093	hemocytin - silkwo
20	152.5	6.0	375	2	A41428	CEF-10 protein pre
21	152.5	6.0	1497	2	I49607	procollagen type V
22	152	6.0	357	2	I38069	gene novH protein
23	148.5	5.8	835	2	JP0076	nel protein - chic
24	148.5	5.8	1487	1	CGHU6C	collagen alpha 1(I
25	148	5.8	488	2	A27353	collagen alpha 1(I
26	146.5	5.8	1464	2	S59856	collagen alpha 1(I
27	146	5.7	349	2	A40551	connective tissue
28	146	5.7	1056	2	A53767	mucin MUC5B, trach
29	145.5	5.7	1042	2	A57534	mucin 5AC (clone L
30	144.5	5.7	1492	2	A40333	collagen alpha 1'(
31	144	5.7	1464	1	CGHU1S	collagen alpha 1(I
32	143	5.6	1486	1	B40333	collagen alpha 1(I
33	142.5	5.6	1496	1	CGHU2V	collagen alpha 2(V
34	141	5.5	1172	1	TSHUP2	thrombospondin 2 p
35	139	5.5	379	2	A35669	gene CYR61 protein
36	138	5.4	2555	2	A40043	notch protein homo
37	137.5	5.4	1746	1	S19694	tenascin precursor
38	137.5	5.4	2318	2	S45306	notch 3 protein -
39	135.5	5.3	197	2	T10081	sperm mitochondria
40	135.5	5.3	4006	2	T09070	probable tenascin
41	134	5.3	1487	2	B41182	collagen alpha 1(I
42	133.5	5.2	1178	1	A39804	thrombospondin pre
43	133	5.2	98	2	I49562	alpha-1 type III c
44	131	5.1	348	2	A40578	beta IG-M2 protein
45	131	5.1	1172	2	A42587	thrombospondin 2 p

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 20:46:19 ; Search time 49 Seconds
(without alignments)
2602.043 Million cell updates/sec

Title: US-10-063-591-82
Perfect score: 2545
Sequence: 1 MVPEVRVLSSLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	2545	100.0	451	9	US-09-965-528-13	Sequence 13, Appl
2	2545	100.0	451	10	US-09-946-374-142	Sequence 142, App
3	2545	100.0	451	12	US-10-206-915-282	Sequence 282, App
4	2545	100.0	451	12	US-10-199-670-282	Sequence 282, App
5	2545	100.0	451	12	US-10-201-858-282	Sequence 282, App
6	2545	100.0	451	12	US-09-969-984-13	Sequence 13, Appl
7	2545	100.0	451	12	US-10-205-890-282	Sequence 282, App
8	2545	100.0	451	12	US-10-208-024-282	Sequence 282, App
9	2545	100.0	451	12	US-10-201-853-282	Sequence 282, App
10	2545	100.0	451	12	US-10-063-745-82	Sequence 82, Appl
11	2545	100.0	451	12	US-10-063-512-82	Sequence 82, Appl
12	2545	100.0	451	12	US-10-063-513-82	Sequence 82, Appl
13	2545	100.0	451	12	US-10-063-515-82	Sequence 82, Appl
14	2545	100.0	451	12	US-10-063-549-82	Sequence 82, Appl
15	2545	100.0	451	12	US-10-063-569-82	Sequence 82, Appl
16	2545	100.0	451	12	US-10-063-551-82	Sequence 82, Appl
17	2545	100.0	451	12	US-10-174-581-282	Sequence 282, App
18	2545	100.0	451	12	US-10-176-483-282	Sequence 282, App
19	2545	100.0	451	12	US-10-176-749-282	Sequence 282, App
20	2545	100.0	451	12	US-10-176-914-282	Sequence 282, App
21	2545	100.0	451	12	US-10-176-915-282	Sequence 282, App
22	2545	100.0	451	12	US-10-006-485A-142	Sequence 142, App
23	2545	100.0	451	12	US-10-013-907A-142	Sequence 142, App
24	2545	100.0	451	12	US-10-015-499A-142	Sequence 142, App
25	2545	100.0	451	12	US-10-063-555-82	Sequence 82, Appl
26	2545	100.0	451	12	US-10-063-563-82	Sequence 82, Appl
27	2545	100.0	451	12	US-10-063-594-82	Sequence 82, Appl
28	2545	100.0	451	12	US-10-063-553-82	Sequence 82, Appl
29	2545	100.0	451	12	US-10-063-554-82	Sequence 82, Appl
30	2545	100.0	451	12	US-10-176-484-282	Sequence 282, App
31	2545	100.0	451	12	US-10-180-550-282	Sequence 282, App
32	2545	100.0	451	12	US-10-183-014-282	Sequence 282, App
33	2545	100.0	451	12	US-10-187-738-282	Sequence 282, App
34	2545	100.0	451	12	US-10-187-740-282	Sequence 282, App
35	2545	100.0	451	12	US-10-187-883-282	Sequence 282, App
36	2545	100.0	451	12	US-10-194-363-282	Sequence 282, App
37	2545	100.0	451	12	US-10-194-460-282	Sequence 282, App
38	2545	100.0	451	12	US-10-194-463-282	Sequence 282, App
39	2545	100.0	451	12	US-10-194-484-282	Sequence 282, App
40	2545	100.0	451	12	US-10-195-884-282	Sequence 282, App
41	2545	100.0	451	12	US-10-195-896-282	Sequence 282, App
42	2545	100.0	451	12	US-10-196-744-282	Sequence 282, App
43	2545	100.0	451	12	US-10-196-755-282	Sequence 282, App
44	2545	100.0	451	12	US-10-196-757-282	Sequence 282, App
45	2545	100.0	451	12	US-10-197-704-282	Sequence 282, App

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 20:45:04 ; Search time 22 Seconds
(without alignments)
1058.332 Million cell updates/sec

Title: US-10-063-591-82
Perfect score: 2545
Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	2136.5	83.9	429	4	US-09-798-051-5	Sequence 5, Appli
2	2032.5	79.9	408	4	US-09-798-051-6	Sequence 6, Appli
3	1543	60.6	426	4	US-09-798-051-2	Sequence 2, Appli
4	1470	57.8	405	4	US-09-798-051-3	Sequence 3, Appli
5	814	32.0	452	4	US-09-798-051-9	Sequence 9, Appli
6	330	13.0	217	4	US-09-152-060-71	Sequence 71, Appl
7	322	12.7	940	2	US-08-938-365-4	Sequence 4, Appli
8	322	12.7	941	1	US-08-343-760A-2	Sequence 2, Appli
9	322	12.7	954	2	US-08-749-169A-3	Sequence 3, Appli
10	322	12.7	954	2	US-09-130-032A-3	Sequence 3, Appli
11	322	12.7	954	4	US-09-866-028-7	Sequence 7, Appli

12	321.5	12.6	955	4	US-09-798-051-8	Sequence 8, Appli
13	288	11.3	283	4	US-09-798-051-7	Sequence 7, Appli
14	272.5	10.7	855	2	US-08-938-365-3	Sequence 3, Appli
15	272	10.7	867	2	US-08-938-365-2	Sequence 2, Appli
16	199.5	7.8	441	3	US-08-985-526-3	Sequence 3, Appli
17	177	7.0	2050	2	US-08-347-594A-2	Sequence 2, Appli
18	177	7.0	2813	4	US-09-381-261A-1	Sequence 1, Appli
19	170	6.7	810	2	US-08-820-170A-34	Sequence 34, Appl
20	170	6.7	810	3	US-09-055-699-34	Sequence 34, Appl
21	170	6.7	810	3	US-09-273-565-34	Sequence 34, Appl
22	170	6.7	810	4	US-09-565-538-34	Sequence 34, Appl
23	170	6.7	810	4	US-09-661-468-34	Sequence 34, Appl
24	170	6.7	810	4	US-09-976-165-34	Sequence 34, Appl
25	166.5	6.5	2813	3	US-08-896-449A-2	Sequence 2, Appli
26	166.5	6.5	2813	3	US-09-132-652-2	Sequence 2, Appli
27	161	6.3	816	2	US-08-820-170A-37	Sequence 37, Appl
28	161	6.3	816	3	US-09-055-699-37	Sequence 37, Appl
29	161	6.3	816	3	US-09-273-565-37	Sequence 37, Appl
30	161	6.3	816	4	US-09-565-538-37	Sequence 37, Appl
31	161	6.3	816	4	US-09-661-468-37	Sequence 37, Appl
32	161	6.3	816	4	US-09-976-165-37	Sequence 37, Appl
33	158.5	6.2	623	3	US-09-029-348-3	Sequence 3, Appli
34	158.5	6.2	626	3	US-09-029-348-2	Sequence 2, Appli
35	155.5	6.1	348	1	US-08-468-847B-14	Sequence 14, Appl
36	152.5	6.0	375	1	US-08-468-847B-13	Sequence 13, Appl
37	152	6.0	357	1	US-08-468-847B-17	Sequence 17, Appl
38	152	6.0	357	4	US-09-253-316-25	Sequence 25, Appl
39	149.5	5.9	1238	3	US-09-214-278-5	Sequence 5, Appli
40	149.5	5.9	1238	4	US-09-855-722-5	Sequence 5, Appli
41	149	5.9	217	4	US-09-602-543-5	Sequence 5, Appli
42	149	5.9	235	4	US-09-602-543-4	Sequence 4, Appli
43	148.5	5.8	1212	3	US-09-214-278-3	Sequence 3, Appli
44	148.5	5.8	1212	4	US-09-855-722-3	Sequence 3, Appli
45	146.5	5.8	1461	4	US-09-585-887-9	Sequence 9, Appli

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 20:39:48 ; Search time 59 Seconds
(without alignments)
2159.812 Million cell updates/sec

Title: US-10-063-591-82
Perfect score: 2545
Sequence: 1 MVPEVRVLSSLLGLALLWFP.....DPGAEGHGQSRQSDQDITKT 451

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2545	100.0	451	3	AAU99382	Aay99382 Human PRO
2	2545	100.0	451	4	AAB66131	Aab66131 Protein o
3	2545	100.0	451	4	AAU29164	Aau29164 Human PRO
4	2545	100.0	451	4	AAB87566	Aab87566 Human PRO
5	2545	100.0	451	4	AAU02749	Aau02749 Novel Hum
6	2545	100.0	451	4	AAB48069	Aab48069 Human ext
7	2545	100.0	451	5	ABG95891	Abg95891 Human sec
8	2545	100.0	451	5	AAU78174	Aau78174 Human cho
9	2545	100.0	451	6	ABU58540	Abu58540 Human PRO

10	2545	100.0	451	6	ABU88088	Abu88088	Novel	hum
11	2545	100.0	451	6	ABU84403	Abu84403	Human	sec
12	2545	100.0	451	6	ABR66277	Abr66277	Human	sec
13	2545	100.0	451	6	ABR65667	Abr65667	Human	sec
14	2545	100.0	451	6	ABU99607	Abu99607	Human	sec
15	2545	100.0	451	6	ABU82846	Abu82846	Human	PRO
16	2545	100.0	451	6	ABU89967	Abu89967	Novel	hum
17	2545	100.0	451	6	ABR68216	Abr68216	Human	sec
18	2545	100.0	451	6	ABU96269	Abu96269	Novel	hum
19	2545	100.0	451	6	ABU92700	Abu92700	Human	sec
20	2545	100.0	451	6	ABO08777	Abo08777	Human	sec
21	2545	100.0	451	6	ABO02829	Abo02829	Human	sec
22	2545	100.0	451	6	ABR74983	Abr74983	Human	sec
23	2545	100.0	451	6	ABR94745	Abr94745	Human	sec
24	2545	100.0	451	6	ABU85718	Abu85718	Human	PRO
25	2545	100.0	451	6	ABU98878	Abu98878	Novel	hum
26	2545	100.0	451	6	ABU98093	Abu98093	Novel	hum
27	2545	100.0	451	6	ABU91799	Abu91799	Novel	hum
28	2545	100.0	451	6	ABU89492	Abu89492	Human	PRO
29	2545	100.0	451	6	ABU86333	Abu86333	Human	sec
30	2545	100.0	451	6	ABU67546	Abu67546	Human	sec
31	2545	100.0	451	6	ABU80574	Abu80574	Human	PRO
32	2545	100.0	451	6	ABU90916	Abu90916	Novel	hum
33	2545	100.0	451	6	ABO33975	Abo33975	Human	sec
34	2545	100.0	451	6	ABR99492	Abr99492	Human	sec
35	2545	100.0	451	6	ABR98882	Abr98882	Human	sec
36	2545	100.0	451	6	ABO16405	Abo16405	Human	sec
37	2545	100.0	451	6	ABR92305	Abr92305	Human	sec
38	2545	100.0	451	6	ABO18946	Abo18946	Human	sec
39	2545	100.0	451	6	ABR78367	Abr78367	Human	sec
40	2545	100.0	451	6	ABU71992	Abu71992	Novel	hum
41	2545	100.0	451	6	ABU85103	Abu85103	Novel	hum
42	2545	100.0	451	6	ABO00242	Abo00242	Novel	hum
43	2545	100.0	451	6	ABO11574	Abo11574	Human	sec
44	2545	100.0	451	6	ABO02219	Abo02219	Human	sec
45	2545	100.0	451	6	ABU88793	Abu88793	Novel	hum